

Genome survey of nematomorph worm *Gordionus alpestris* using NGS

B.D. Efeykin, S.E. Spiridonov

Center of parasitology, A.N. Severtsov Institute of Ecology and Evolution, Russian Academy of Sciences,
Moscow, Russia bocha19@yandex.ru

K.V. Mikhailov, V.V. Aleoshin

Belozersky Institute of Physico-Chemical Biology M.V. Lomonosov Moscow State University,
Moscow, Russia aleshin@genebee.msu.su

Y.V. Panchin

A.A. Kharkevich Institute for Information Transmission Problems, Russian Academy of Sciences,
Moscow, Russia ypanchin@yahoo.com

Horse-hair worms or nematomorphs (Nematomorpha) are worm-like organisms parasitizing on larval stages of different arthropods. No whole genomes were previously reported for any members of Nematomorpha, and the position of this phylum within Ecdysozoa has remained largely uncertain.

The DNA of the nematomorph *Gordionus alpestris*, collected in West Caucasus, was extracted and sequenced on the Illumina HiSeq 2000. Draft genome was assembled using the velvet assembler program from 60M read pairs, achieving at least twenty-fold coverage and N50 of 4050. The draft genome of *Gordionus alpestris* is estimated to be around 250 Mb.

To estimate the quality and completeness of the draft assembly we searched all ORFs in the assembly against Pfam database and compared the number of Pfam hits to other genome projects. We found 4220 Pfam hits in draft assembly of *Gordionus*, which is close to the number of domains in well annotated genomes (3634 in *C. elegans*; 5081 in *Danio rerio* and 4042 in *D. melanogaster*).

A set of 77 ribosomal proteins was selected to determine phylogenetic position of Nematomorpha, and a wide range of ecdysozoan organisms was sampled to construct the alignments. The tree was built by the maximum likelihood method implemented in RAxML; node support was estimated with 100 bootstrap replicates. The result of phylogenetic analysis revealed Nematomorpha as a group sister to Nematoda with moderate statistical support (Fig. below).

